

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Barnwell, John
- (ii) TITLE OF INVENTION: Plasmodium vivax Blood Stage Antigens, Monoclonal Antibodies, and Diagnostic Assays
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Darby and Darby
  - (B) STREET: 805 Third Ave.
  - (C) CITY: New York
  - (D) STATE: New York
  - (E) COUNTRY: USA
  - (F) ZIP: 10022-7513
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: US
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Gogoris, Adda
  - (B) REGISTRATION NUMBER: 29,714
  - (C) REFERENCE/DOCKET NUMBER: 5986/07686
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (212)527-7700
  - (B) TELEFAX: (212)753-6237
  - (C) TELEX: 236687

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3337 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Plasmodium vivax

(vii) IMMEDIATE SOURCE:

(B) CLONE: PvMB3.3.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGT AAAGTAACAA CTATGTTTC GTATCTATAT ATAACCTTAC TAATTTTATC 60  
TTTTGCTTTT CTTTAAATTC ATGCTTCAAC AGTAAGATAA AAATAATCTA TAAAAACTGC 120  
TATATATACA TATATATTCA TAAGTGGCAT TTGTGAATTG CGATCATTTA AATTACGTA 180  
AAAACAATAT TGAAAAAAT TTTTTTTTTT TTTTTTTTTT TGTCTACAG AACGATTTAG 240  
AATTGGAAAA TGCTTCTGAT GATGTTGTAG AGGTGGAGGA TCCTTCAAAC GACGGTTTAG 300  
AATTAGAAGA GGAAATTTT GATGAGAATT CAGGTGATGA TGAACTCTT TTAGATGCTA 360  
CCCCGAAGA TGAATTTGCC TTAACAGATT TGCCAATTGA AGACGATGAG GAAGTCAACG 420  
AAACGTTAGA TGGAGGTGAA TCATTAGGAG AGGTTTCCAC TGAAGATATG GAAACAGAAG 480  
ATGGCTCAAC AGATGATACG GAAACAGAAG AAGGACTACC TGGTGATATG GAAGGAGAAG 540  
AAGAAGCTGG CGATATGGAA GCAGGGGAAG AAGCTGGTGA TTTGGAAGCA GGGGAAGAAA 600  
CTGGCGATTT GGAAGCAGGG GAAGAACTG GCGATTTGGA AGCAGGGGAA GAAGCTGGTG 660  
ATTTGGAAGC AGGGGAAGAA ACTGGCGATT TGGAAGCAGG GGAAGAACT GGAGATGCGG 720  
AAACTGAAGA AGGAGCAACT GGAGATGCGG AAACGAAAA TGGAGCAACT GTGTATGTAG 780  
ACACAGAAGA TAGTTCAGCT GATGGAGCAG AAAAAGTACA TCTTCCTGCT CAAGAAAATG 840  
TACAACCTGC CGATAGTAAT GATGCCCTCT TTGGAAGTAT TTTGGATAAA GATATAATTT 900  
TTGATCATAT TAAAGATTTT GAGCCACTAT TCGAACAAAT TGTGGCGGGT ACTGCTAAAC 960  
ATGTTACGGG ACAAGAATTG CCAATGAAAC CTGTACCATT ACCAGTGGCA GAAGAGCCCC 1020  
CGCAAGTACC AGCGGAAGAA TTAGATGCCA CTCCAGAGGA TGAATTCGA TTAGATGTTA 1080  
CAGAATCTCC CGAGGAAGTA GAATTAGTAT TAGATGAAGA GGCAACTGAA GAAGAATCAA 1140  
CGGAAGTGGG ACCAACGGAA GAAGGACCAA CCGAAGAATT AGATGCCACT CCAGAGGATG 1200  
GATTTGCGAT TAGACGAAAC TGCAGAAGGA GAAACAGAAG AAACGTAGAG GGAGAAGAAA 1260  
CAGAAGAAGC TGCAGAAGGA GAAGTATCAG AAGAACTCC AGAAGGAGAA GAAGAGTTAG 1320

|            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------|
| AGGCAACTCC | AGAGGATGAT | TTCGCATTAG | ATGGAACTAC | ATTAGAAGAA | ACCGAAGAAA | 1380 |
| CTGCAGAAGG | AGAAGAAACC | GTAGAGGGAG | AAGAAACCGT | AGAGGGAGAA | GAAACCGTAG | 1440 |
| AGGGAGAAGA | AGCTGCAGAA | GGAGAAGAAG | AGTTAGAGGC | AACTCCAGAG | GATGACTTCC | 1500 |
| AATTAGAAGA | ACCATCAGGA | GAAGGAGAAG | GGGAAGGAGA | AGGAGAAGGG | GAAGGAGAAG | 1560 |
| GAGAAGCGTT | AGTAGCAGTG | CCAGTAGTGG | CCGAACCGGT | AGAAGTAGTG | ACTCCTGCTC | 1620 |
| AGCCTGTCAA | ACCAATGGTC | GCTCCAACGG | CAGATGAAAC | TTTATTCGTT | GATATCTTAG | 1680 |
| ATAACGATTT | AACGTATGCA | GACATTACAT | CCTTTGAGCC | ATTATTTAAA | CAAATCCTCA | 1740 |
| AGGATCCTGA | TGCAGGAGAG | GCTGTAACAG | TACCATCAAA | GGAAGCACCT | GTACAAGTAC | 1800 |
| CAGTGGCAGT | AGGGCCCGCG | CAAGAAGTGC | CAACGGAAGA | ATTGATGCAA | CTCCAAGAGG | 1860 |
| ACGATTTCGA | ATTAGAAGGA | ACTGCAGAAG | CTCCAGAGGA | AGGAGAATTA | GTATTAGAAG | 1920 |
| GAGAAGGAGA | ACCAACGGAA | GAAGAGCCAA | GAGAAGGAGA | GCCAACAGAA | GGAGAAGTGC | 1980 |
| CAGAGAAGA  | ATTAGAGGCA | ACTCCAGAGG | ACGATTTCGA | ATTAGAAGAA | CCAACAGGAG | 2040 |
| AAGAAGTAGA | AGAAACCGTA | GAGGGCGAAG | AAACTGCAGA | AGGAGAAGAA | GTGGAAGAGG | 2100 |
| TACCTGCAGA | AGTAGAAGAA | GTGGAAGAGG | TACCTGCAGA | AGTAGAAGAA | GTGGAAGAGG | 2160 |
| TACCGAAGA  | AGTAGAAGAG | GTACCCGCAG | AAGTAGAAGA | AGTGGAAGAG | GTACCAGAAG | 2220 |
| AAGTGGAAGA | GGTACCAGAA | GAAGTGGAAG | AGGTACCAGA | AGAAGTGGAA | GAGGTACCAG | 2280 |
| AAGAAGTGA  | AGAAGTGGAA | GAAGTAGAAG | AAGTAGAGGT | ACCAGCGGTA | GTAGAAGTAG | 2340 |
| AAGTACCAGC | GGTAGTAGAA | GAAGAGGTGC | CAGAAGAAGT | AGAAGAAGAA | GAAGAAGAGG | 2400 |
| AAGAACCACT | AGAGGAAGAA | GATGTATTAC | AATTAGTAAT | ACCATCGGAA | GAAGATATAC | 2460 |
| AATTAGACAA | ACCAAAGAAA | GACGAATTAG | GCTCTGGAAT | TTTATCTATC | ATCGACATGC | 2520 |
| ACTACCAAGA | CGTTCCAAAG | GAATTTATGG | AAGAAGAAGA | AGAAACTGCA | GTGTATCCAT | 2580 |
| TGAAACCAGA | AGATTTTGCA | AAGGAAGATT | CACAATCTAC | AGAATGGCTC | ACATTCATTC | 2640 |
| AAGGCCTAGA | AGGCGACTGG | GAACGATTAG | AAGTGAGCTT | AAATAAGGCT | AGAGAAAGAT | 2700 |
| GGATGGAACA | AAGAAATAAA | GAATGGGCTG | GCTGGCTTCG | CTTAATTGAA | AATAAATGGT | 2760 |
| CAGAATATAG | TCAAATTTCA | ACAAAAGGAA | AGGACCCAGC | TGGTTTGAGA | AAACGAGAGT | 2820 |
| GGAGCGACGA | GAAATGGAAA | AAATGGTTTA | AAGCAGAAGT | CAAATCCCAA | ATTGATTAC  | 2880 |
| ACTTGAAAAA | ATGGATGAAC | GACACTCATT | CCAATTTATT | TAAAATTCTT | GTGAAAGATA | 2940 |

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TGTCAACAATT TGAAAACAAG AAAACCAAAG AATGGTTAAT GAATCACTGG AAAAAGAACG 3000  
 AACGGGGTTA TGGTTCTGAA TCATTGGAAG TTATGACCAC ATCAAAATTA TTAAATGTGG 3060  
 CTAAGAGTCG AGAATGGTAC CGTGCCAATC CTAATATAAA TAGAGAAAGA AGAGAACTCA 3120  
 TGAAATGGTT TCTCCTAAAA GAAAACGAAT ATTTAGGACA AAGAATGGAA AAAATGGACT 3180  
 CATTGGAAAA AAGTTAAATT TTTGTGTTC AATTCAATGT GTACAACATT TTCTGGAAAA 3240  
 CGCCTAACCA AGGAAGAATG GAATCAATTT GTTAATGAAA TAAAAGTTTG AATTATAGAA 3300  
 AAAAGAACAG ATTATTCTCT TATAAAATTA ATAATTC 3337

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1018 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: C-terminal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Plasmodium vivax

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PvMB3.3.1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asn Ser Gly Lys Val Thr Thr Met Val Ser Tyr Leu Tyr Ile Thr Leu  
 1 5 10 15

Leu Ile Leu Ser Phe Ala Phe Leu Leu Ile His Ala Ser Thr Asn Asp  
 20 25 30

Leu Glu Leu Glu Asn Ala Ser Asp Asp Val Val Glu Val Glu Asp Pro  
 35 40 45

Ser Asn Asp Gly Leu Glu Leu Glu Glu Asn Phe Asp Glu Asn Ser  
 50 55 60

Gly Asp Asp Glu Thr Leu Leu Asp Ala Thr Pro Glu Asp Asp Phe Ala  
 65 70 75 80

Leu Thr Asp Leu Pro Ile Glu Asp Asp Glu Glu Val Asn Glu Thr Leu

85

90

95

Asp Gly Gly Glu Ser Leu Gly Glu Val Ser Thr Glu Asp Met Glu Thr  
 100 105 110  
 Glu Asp Gly Ser Thr Asp Asp Thr Glu Thr Glu Glu Gly Leu Pro Gly  
 115 120 125  
 Asp Met Glu Gly Glu Glu Glu Ala Gly Asp Met Glu Ala Gly Glu Glu  
 130 135 140  
 Ala Gly Asp Leu Glu Ala Gly Glu Glu Thr Gly Asp Leu Glu Ala Gly  
 145 150 155 160  
 Glu Glu Thr Gly Asp Leu Glu Ala Gly Glu Glu Ala Gly Asp Leu Glu  
 165 170 175  
 Ala Gly Glu Glu Thr Gly Asp Leu Glu Ala Gly Glu Glu Thr Gly Asp  
 180 185 190  
 Ala Glu Thr Glu Glu Gly Ala Thr Gly Asp Ala Glu Thr Glu Asn Gly  
 195 200 205  
 Ala Thr Val Tyr Val Asp Thr Glu Asp Ser Ser Ala Asp Gly Ala Glu  
 210 215 220  
 Lys Val His Val Pro Ala Gln Glu Asn Val Gln Pro Ala Asp Ser Asn  
 225 230 235 240  
 Asp Ala Leu Phe Gly Ser Ile Leu Asp Lys Asp Ile Ile Phe Asp His  
 245 250 255  
 Ile Lys Asp Phe Glu Pro Leu Phe Glu Gln Ile Val Ala Gly Thr Ala  
 260 265 270  
 Lys His Val Thr Gly Gln Glu Leu Pro Met Lys Pro Val Pro Leu Pro  
 275 280 285  
 Val Ala Glu Glu Pro Ala Gln Val Pro Ala Glu Glu Leu Asp Ala Thr  
 290 295 300  
 Pro Glu Asp Asp Phe Ala Leu Asp Val Thr Glu Ser Pro Glu Glu Val  
 305 310 315 320  
 Glu Leu Val Leu Asp Glu Glu Ala Thr Glu Glu Glu Ser Thr Glu Val  
 325 330 335  
 Gly Pro Thr Glu Glu Gly Pro Thr Glu Glu Leu Asp Ala Thr Pro Glu  
 340 345 350  
 Asp Gly Phe Arg Ile Arg Arg Asn Cys Arg Arg Arg Asn Arg Arg Asn  
 355 360 365  
 Val Glu Gly Glu Glu Thr Glu Glu Ala Ala Glu Gly Glu Val Ser Glu

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370

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Glu Thr Pro Glu Gly Glu Glu Glu Leu Glu Ala Thr Pro Glu Asp Asp  
385 390 395 400

Phe Ala Leu Asp Gly Thr Thr Leu Glu Glu Thr Glu Glu Thr Ala Glu  
405 410 415

Gly Glu Glu Thr Val Glu Gly Glu Glu Thr Val Glu Gly Glu Glu Thr  
420 425 430

Val Glu Gly Glu Glu Ala Ala Glu Gly Glu Glu Glu Leu Glu Ala Thr  
435 440 445

Pro Glu Asp Asp Phe Gln Leu Glu Glu Pro Ser Gly Glu Gly Glu Gly  
450 455 460

Glu Gly Glu Gly Glu Gly Glu Gly Glu Gly Glu Ala Leu Val Ala Val  
465 470 475 480

Pro Val Val Ala Glu Pro Val Glu Val Val Thr Pro Ala Gln Pro Val  
485 490 495

Lys Pro Met Val Ala Pro Thr Ala Asp Glu Thr Leu Phe Val Asp Ile  
500 505 510

Leu Asp Asn Asp Leu Thr Tyr Ala Asp Ile Thr Ser Phe Glu Pro Leu  
515 520 525

Phe Lys Gln Ile Leu Lys Asp Pro Asp Ala Gly Glu Ala Val Thr Val  
530 535 540

Pro Ser Lys Glu Ala Pro Val Gln Val Pro Val Ala Val Gly Pro Ala  
545 550 555 560

Gln Glu Val Pro Thr Glu Glu Leu Met Gln Leu Gln Glu Asp Asp Phe  
565 570 575

Glu Leu Glu Gly Thr Ala Glu Ala Pro Glu Glu Gly Glu Leu Val Leu  
580 585 590

Glu Gly Glu Gly Glu Pro Thr Glu Glu Glu Pro Arg Glu Gly Glu Pro  
595 600 605

Thr Glu Gly Glu Val Pro Glu Glu Glu Leu Glu Ala Thr Pro Glu Asp  
610 615 620

Asp Phe Glu Leu Glu Glu Pro Thr Gly Glu Glu Val Glu Glu Thr Val  
625 630 635 640

Glu Gly Glu Glu Thr Ala Glu Gly Glu Glu Val Glu Glu Val Pro Ala  
645 650 655

Glu Val Glu Glu Val Glu Glu Val Pro Ala Glu Val Glu Glu Val Glu

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Glu Val Pro Glu Glu Val Glu Glu Val Pro Ala Glu Val Glu Glu Val  
675 680 685

Glu Glu Val Pro Glu Glu Val Glu Glu Val Pro Glu Glu Val Glu Glu  
690 695 700

Val Pro Glu Glu Val Glu Glu Val Pro Glu Glu Val Glu Glu Val Glu  
705 710 715 720

Glu Val Glu Glu Val Glu Val Pro Ala Val Val Glu Val Glu Val Pro  
725 730 735

Ala Val Val Glu Glu Glu Val Pro Glu Glu Val Glu Glu Glu Glu  
740 745 750

Glu Glu Glu Pro Val Glu Glu Glu Asp Val Leu Gln Leu Val Ile Pro  
755 760 765

Ser Glu Glu Asp Ile Gln Leu Asp Lys Pro Lys Lys Asp Glu Leu Gly  
770 775 780

Ser Gly Ile Leu Ser Ile Ile Asp Met His Tyr Gln Asp Val Pro Lys  
785 790 795 800

Glu Phe Met Glu Glu Glu Glu Thr Ala Val Tyr Pro Leu Lys Pro  
805 810 815

Glu Asp Phe Ala Lys Glu Asp Ser Gln Ser Thr Glu Trp Leu Thr Phe  
820 825 830

Ile Gln Gly Leu Glu Gly Asp Trp Glu Arg Leu Glu Val Ser Leu Asn  
835 840 845

Lys Ala Arg Glu Arg Trp Met Glu Gln Arg Asn Lys Glu Trp Ala Gly  
850 855 860

Trp Leu Arg Leu Ile Glu Asn Lys Trp Ser Glu Tyr Ser Gln Ile Ser  
865 870 875 880

Thr Lys Gly Lys Asp Pro Ala Gly Leu Arg Lys Arg Glu Trp Ser Asp  
885 890 895

Glu Lys Trp Lys Lys Trp Phe Lys Ala Glu Val Lys Ser Gln Ile Asp  
900 905 910

Ser His Leu Lys Lys Trp Met Asn Asp Thr His Ser Asn Leu Phe Lys  
915 920 925

Ile Leu Val Lys Asp Met Ser Gln Phe Glu Asn Lys Lys Thr Lys Glu  
930 935 940

Trp Leu Met Asn His Trp Lys Lys Asn Glu Arg Gly Tyr Gly Ser Glu

945

955

960

Ser Phe Glu Val Met Thr Thr Ser Lys Leu Leu Asn Val Ala Lys Ser  
965 970 975

Arg Glu Trp Tyr Arg Ala Asn Pro Asn Ile Asn Arg Glu Arg Arg Glu  
980 985 990

Leu Met Lys Trp Phe Leu Leu Lys Glu Asn Glu Tyr Leu Gly Gln Arg  
995 1000 1005

Met Glu Lys Met Asp Ser Leu Glu Lys Ser  
1010 1015

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